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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/888,370

DATE: 12/04/2001  
 TIME: 08:52:35

Input Set : N:\Crf3\RULE60\09888370.raw  
 Output Set: N:\CRF3\12042001\I888370.raw

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## SEQUENCE LISTING

3 (1) GENERAL INFORMATION:  
 5 (i) APPLICANT: Glimcher, Laurie H. et al.  
 7 (ii) TITLE OF INVENTION: Human c-Maf Compositions and  
 8 Methods of Use Thereof  
 10 (iii) NUMBER OF SEQUENCES: 2  
 12 (iv) CORRESPONDENCE ADDRESS:  
 13 (A) ADDRESSEE: LAHIVE & COCKFIELD, LLP  
 14 (B) STREET: 28 State Street  
 15 (C) CITY: Boston  
 16 (D) STATE: Massachusetts  
 17 (E) COUNTRY: USA  
 18 (F) ZIP: 02109  
 20 (v) COMPUTER READABLE FORM:  
 21 (A) MEDIUM TYPE: Floppy disk  
 22 (B) COMPUTER: IBM PC compatible  
 23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25  
 26 (vi) CURRENT APPLICATION DATA:  
 C--> 27 (A) APPLICATION NUMBER: US/09/888,370  
 C--> 28 (B) FILING DATE: 22-Jun-2001  
 29 (C) CLASSIFICATION:  
 31 (vii) PRIOR APPLICATION DATA:  
 32 (A) APPLICATION NUMBER: US/09/086,010  
 33 (B) FILING DATE:  
 34 (A) APPLICATION NUMBER: 09/030,579  
 35 (B) FILING DATE: 2-FEB-1998  
 37 (viii) ATTORNEY/AGENT INFORMATION:  
 38 (A) NAME: Kara, Catherine J.  
 39 (B) REGISTRATION NUMBER: 41,106  
 40 (C) REFERENCE/DOCKET NUMBER: HUI-027CP  
 42 (ix) TELECOMMUNICATION INFORMATION:  
 43 (A) TELEPHONE: (617)227-7400  
 44 (B) TELEFAX: (617)742-4214  
 47 (2) INFORMATION FOR SEQ ID NO: 1:  
 49 (i) SEQUENCE CHARACTERISTICS:  
 50 (A) LENGTH: 1203 base pairs  
 51 (B) TYPE: nucleic acid  
 52 (C) STRANDEDNESS: single  
 53 (D) TOPOLOGY: linear  
 55 (ii) MOLECULE TYPE: cDNA  
 58 (ix) FEATURE:  
 59 (A) NAME/KEY: CDS  
 60 (B) LOCATION: 1..1203  
 63 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 65 ATG GCA TCA GAA CTG GCA ATG AGC AAC TCC GAC CTG CCC ACC AGT CCC 48  
 66 Met Ala Ser Glu Leu Ala Met Ser Asn Ser Asp Leu Pro Thr Ser Pro



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133 CGG CAG CTG CGC GGG GTC AGC AAG GAG GAG GTG ATC CGG CTG AAG CAG      864
134 Arg Gln Leu Arg Gly Val Ser Lys Glu Glu Val Ile Arg Leu Lys Gln
135      275      280      285
137 AAG AGG CGG ACC CTG AAA AAC CGC GGC TAT GCC AAG TCC TGC CGC TTC      912
138 Lys Arg Arg Thr Leu Lys Asn Arg Gly Tyr Ala Lys Ser Cys Arg Phe
139      290      295      300
141 AAG AGG GTG CAG CAG AGA CAC GTC CTG GAG TCG GAG AAG AAC CAG CTG      960
142 Lys Arg Val Gln Gln Arg His Val Leu Glu Ser Glu Lys Asn Gln Leu
143 305      310      315      320
145 CTG CAG CAA GTC GAC CAC CTC AAG CAG GAG ATC TCC AGG CTG GTG CGC      1008
146 Leu Gln Gln Val Asp His Leu Lys Gln Glu Ile Ser Arg Leu Val Arg
147      325      330      335
149 GAG AGG GAC GCG TAC AAG GAG AAA TAC GAG AAG TTG GTG AGC AGC GGC      1056
150 Glu Arg Asp Ala Tyr Lys Glu Lys Tyr Glu Lys Leu Val Ser Ser Gly
151      340      345      350
153 TTC CGA GAA AAC GGC TCG AGC AGC GAC AAC CCG TCC TCT CCC GAG TTT      1104
154 Phe Arg Glu Asn Gly Ser Ser Ser Asp Asn Pro Ser Ser Pro Glu Phe
155      355      360      365
157 TTC ATA ACT GAG CCC ACT CGC AAG TTG GAG CCA TCA GTG GGA TAC GCC      1152
158 Phe Ile Thr Glu Pro Thr Arg Lys Leu Glu Pro Ser Val Gly Tyr Ala
159      370      375      380
161 ACA TTT TGG AAG CCC CAG CAT CGT GTA CTT ACC AGT GTG TTC ACA AAA      1200
162 Thr Phe Trp Lys Pro Gln His Arg Val Leu Thr Ser Val Phe Thr Lys
163 385      390      395      400
165 TGA      1203
170 (2) INFORMATION FOR SEQ ID NO: 2:
172 (i) SEQUENCE CHARACTERISTICS:
173 (A) LENGTH: 400 amino acids
174 (B) TYPE: amino acid
175 (D) TOPOLOGY: linear
177 (ii) MOLECULE TYPE: protein
179 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
181 Met Ala Ser Glu Leu Ala Met Ser Asn Ser Asp Leu Pro Thr Ser Pro
182 1      5      10      15
184 Leu Ala Met Glu Tyr Val Asn Asp Phe Asp Leu Met Lys Phe Glu Val
185      20      25      30
187 Lys Lys Glu Pro Val Glu Thr Asp Arg Ile Ile Ser Gln Cys Gly Arg
188      35      40      45
190 Leu Ile Ala Gly Gly Ser Leu Ser Ser Thr Pro Met Ser Thr Pro Cys
191      50      55      60
193 Ser Ser Val Pro Pro Ser Pro Ser Phe Ser Ala Pro Ser Pro Gly Ser
194 65      70      75      80
196 Arg Gly Glu Gln Lys Ala His Leu Glu Asp Tyr Tyr Trp Met Thr Gly
197      85      90      95
199 Tyr Pro Gln Gln Leu Asn Pro Glu Ala Leu Gly Phe Ser Pro Glu Asp
200      100      105      110
202 Ala Val Glu Ala Leu Ile Ser Asn Ser His Gln Leu Arg Gly Gly Phe
203      115      120      125
205 Asp Gly Tyr Ala Arg Gly Ala Gln Gln Leu Ala Ala Ala Ala Gly Ala

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206	130	135	140
208	Gly Ala Gly Ala Ser Leu Gly Gly Ser Gly Glu Glu Met Gly Pro Ala		
209	145	150	155
211	Ala Ala Val Val Ser Ala Val Ile Ala Ala Ala Ala Gln Ser Gly		
212		165	170
214	Ala Gly Pro His Tyr His His His His His His Ala Ala Gly His His		
215		180	185
217	His His Pro Thr Ala Gly Ala Pro Gly Ala Ala Gly Ser Ala Ala Ala		
218		195	200
220	Ser Ala Gly Gly Ala Gly Gly Ala Gly Gly Gly Gly Pro Ala Ser Val		
221		210	215
223	Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Ala		
224	225	230	235
226	Gly Ala Leu His Pro His His Ala Ala Gly Gly Leu His Phe Asp Asp		
227		245	250
229	Arg Phe Ser Asp Glu Gln Leu Val Thr Met Ser Val Arg Asp Trp Asn		
230		260	265
232	Arg Gln Leu Arg Gly Val Ser Lys Glu Glu Val Ile Arg Leu Lys Gln		
233		275	280
235	Lys Arg Arg Thr Leu Lys Asn Arg Gly Tyr Ala Lys Ser Cys Arg Phe		
236		290	295
238	Lys Arg Val Gln Gln Arg His Val Leu Glu Ser Glu Lys Asn Gln Leu		
239	305	310	315
241	Leu Gln Gln Val Asp His Leu Lys Gln Glu Ile Ser Arg Leu Val Arg		
242		325	330
244	Glu Arg Asp Ala Tyr Lys Glu Lys Tyr Glu Lys Leu Val Ser Ser Gly		
245		340	345
247	Phe Arg Glu Asn Gly Ser Ser Ser Asp Asn Pro Ser Ser Pro Glu Phe		
248		355	360
250	Phe Ile Thr Glu Pro Thr Arg Lys Leu Glu Pro Ser Val Gly Tyr Ala		
251		370	375
253	Thr Phe Trp Lys Pro Gln His Arg Val Leu Thr Ser Val Phe Thr Lys		
254	385	390	395
			400

**VERIFICATION SUMMARY**

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L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]